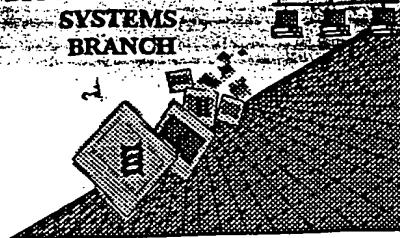




BIOTECHNOLOGY  
SYSTEMS  
BRANCH

## RAW SEQUENCE LISTING ERROR REPORT



The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/836,911

Source: O I P E

Date Processed by STIC: 5/3/2001

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
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FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: [patin21help@uspto.gov](mailto:patin21help@uspto.gov) or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: [patin3help@uspto.gov](mailto:patin3help@uspto.gov) or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

### **Checker Version 3.0**

The Checker Version 3.0 application is a state-of the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO).

Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:  
<http://www.uspto.gov/web/offices/pac/checker>



OIE

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/09/836,911

DATE: 05/03/2001  
TIME: 15:56:14

Input Set : A:\402iseq.001  
Output Set: N:\CRF3\05032001\I836911.raw

Does Not Comply  
Corrected Diskette Needed

PS

## SEQUENCE LISTING

C--> 4 (1) GENERAL INFORMATION:  
5 (i) APPLICANT: Hadlaczky, Gyula  
6 Szalay, Aladar  
C--> 9 (ii) TITLE OF INVENTION: ARTIFICIAL CHROMOSOMES, USES THEREOF  
10 AND METHODS FOR PREPARING ARTIFICIAL CHROMOSOMES  
12 (iii) NUMBER OF SEQUENCES: 34  
14 (iv) CORRESPONDENCE ADDRESS:  
15 (A) ADDRESSEE: Heller Ehrman White & McAuliffe  
16 (B) STREET: 4350 La Jolla Village Drive, 6th Floor  
17 (C) CITY: San Diego  
18 (D) STATE: CA  
19 (E) COUNTRY: USA  
20 (F) ZIP: 92122  
22 (v) COMPUTER READABLE FORM:  
23 (A) MEDIUM TYPE: Diskette  
24 (B) COMPUTER: IBM Compatible  
25 (C) OPERATING SYSTEM: DOS  
26 (D) SOFTWARE: FastSEQ Version 1.5  
28 (vi) CURRENT APPLICATION DATA:  
29 (A) APPLICATION NUMBER: US/09/836,911  
C--> 30 (B) FILING DATE: 17-Apr-2001  
50 (C) CLASSIFICATION:  
C--> 47 (vii) PRIOR APPLICATION DATA:  
33 (A) APPLICATION NUMBER: 08/835,682  
34 (B) FILING DATE: 10-APR-1997  
38 (A) APPLICATION NUMBER: 08/695,191  
39 (B) FILING DATE: 07-AUG-1996  
43 (A) APPLICATION NUMBER: 08/682,080  
44 (B) FILING DATE: 15-JUL-1996  
48 (A) APPLICATION NUMBER: 08/629,822  
49 (B) FILING DATE: 10-APR-1996  
52 (viii) ATTORNEY/AGENT INFORMATION:  
53 (A) NAME: Seidman, Stephanie L  
54 (B) REGISTRATION NUMBER: 33,779  
55 (C) REFERENCE/DOCKET NUMBER: 24601-402I  
58 (ix) TELECOMMUNICATION INFORMATION:  
59 (A) TELEPHONE: 858-450-8403  
60 (B) TELEFAX: 858-587-5360  
61 (C) TELEX:  
63 (2) INFORMATION FOR SEQ ID NO: 1:  
65 (i) SEQUENCE CHARACTERISTICS:  
66 (A) LENGTH: 1293 base pairs  
67 (B) TYPE: nucleic acid  
68 (C) STRANDEDNESS: single  
69 (D) TOPOLOGY: linear  
71 (ii) MOLECULE TYPE: Genomic DNA

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/09/836,911

DATE: 05/03/2001  
TIME: 15:56:14

Input Set : A:\402iseq.001  
Output Set: N:\CRF3\05032001\I836911.raw

72 (iii) HYPOTHETICAL: NO  
 C--> 73 (iv) ANTI-SENSE: NO  
 W--> 74 (v) FRAGMENT TYPE:  
 75 (vi) ORIGINAL SOURCE:  
 76 (ix) FEATURE:  
 78 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:  
 80 GAATTCATCA TTTTCANGT CCTCAAGTGG ATGTTTCTCA TTTNCCATGA TTTTAAGTTT 60  
 81 TCTGCCATA TTCCTGGTCC TACAGTGTGC ATTTCTCCAT TTTNCACGTT TTNCAGTGAT 120  
 82 TTCGTCATTT TCAAGTCCTC AAGTGGATGT TTCTCATTNN CCATGAATT CAGTTTCTN 180  
 83 GCCATATTCC ACGTCCTACA GNGGACATTT CAAATTTNC CACCTTTTC AGTTTCCCTC 240  
 84 GCCATATTTC ACGTCCTAAA ATGTGTATT CTCGTTTNC GTGATTTCAGT GTTTTCTCGC 300  
 85 CAGATTCCAG GTCCTATAAT GTGCATTCTC CATTNNACG GTTTTCAGT GATTTCGTCA 360  
 86 TTTTTCAAG TCGGCAAGTG GATGTTTCTC ATTTNCCATG ATTTNCAGTT TTCTTGNAAT 420  
 87 ATTCCATGTC CTACAATGAT CATTTTAAT TTCCACCTT TTCATTTC CACGCCATAT 480  
 88 TTCATGTCCT AAAGTGTATA TTTCTCCTT TCCGGATTTC TCAGTTTCTC CGCCATATT 540  
 89 CAGGTCCTAC AGTGTGCATT CCTCATTTC CACCTTTTC ACTGATTTCG TCATTTCAGT 600  
 90 AGTCGTCAAC TGGATCTTC TAATTTCCA TGATTTTCAGT TTATCTGTC ATATTCCATG 660  
 91 TCCTCAGTG GACATTCTA AATTTCCA CTTTTCAAT TTTTCTCGAC ATATTGACG 720  
 92 TGCTAAAGTG TGTATTTCTT ATTTCCGTG ATTTTCAGTT TTCTGCCAT ATTCCAGGTC 780  
 93 CTAATAGTGT GCATTCTA TTTTCACGT TTTCAGTGA TTTCGTCATT TTTCCAGTT 840  
 94 GTCAAGGGGA TGTTTCTCAT TTTCCATGAG TGTCAGTTT CTTGCTATAT TCCATGTCC 900  
 95 ACAGTGACAT TTCTAAATAT TATACTTT TCAGTTTTC TCACCATATT TCACGTCC 960  
 96 AAGTATATAT TTCTCATTTC CCCTGATTTC CAGTTTCCCTT GCCATATTCC AGGTCC 1020  
 97 GTGTGCATT TCTCATTTC ACGTTTTCAGT GAAATTCTT CATTTCAGT GGCCTCAAAT 1080  
 98 GGATGTTTCT CATTTCAT GATTTTCAGT TTCTTGCCA TATACCATGT CCTACAGTGG 1140  
 99 ACATTTCTAA ATTATCCAC TTTTCAGTT TTCTCGGC ACATTCACG TCCTAAAGTG 1200  
 100 TGTATTTCTA ATTTTCAGTG ATTTTCAGTT TTCTCGCCAT ATTCCAGGAC CTACAGTGTG 1260  
 101 CATTCTCAT TTTTCAGTT TTCTCAGTGAATTC 1293  
 103 (2) INFORMATION FOR SEQ ID NO: 2:  
 105 (i) SEQUENCE CHARACTERISTICS:  
 106 (A) LENGTH: 1044 base pairs  
 107 (B) TYPE: nucleic acid  
 108 (C) STRANDEDNESS: single  
 109 (D) TOPOLOGY: linear  
 111 (ii) MOLECULE TYPE: Genomic DNA  
 112 (iii) HYPOTHETICAL: NO  
 C--> 113 (iv) ANTI-SENSE: NO  
 W--> 114 (v) FRAGMENT TYPE:  
 115 (vi) ORIGINAL SOURCE:  
 116 (ix) FEATURE:  
 118 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:  
 120 AGGCCTATGG TGAAAAAGGA AATATCTTCC CCTGAAAAGT AGACAGAAGG ATTCTCAGAA 60  
 121 TCTTATTTGT GATGTGCGCC CCTCAACTAA CAGTGTGAA GCTTTCTTT GATAGAGCAG 120  
 122 TTTTGAAACA CTCTTTTGT AAAATCTGCA AGAGGATATT TGGATAGCTT TGAGGATTTC 180  
 123 CGTTGGAAAC GGGATTGTCT TCATATAAAC CCTAGACAGA AGCATCTCA GAAGCTTCAT 240  
 124 TGGGATGTTT CAGTTGAAGT CACAGTGTG AACAGTCCC TTTCATAGAG CAGGTTTGAA 300  
 125 ACACTCTTT TTGTAGTATC TGGAGTGGAA CATTGGAGC GATCTCAGGA CTGCGGTGAA 360  
 126 AAAGGAAATA TCTTCCAATA AAAGCTAGAT AGAGGCAATG TCAGAAACCT TTTTCATGAT 420  
 127 GTATCTACTC AGCTAACAGA GTTGAACCTT CCTTTGAGAG AGCAGTTTG AAACACTCTT 480

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/09/836,911

DATE: 05/03/2001  
TIME: 15:56:14

Input Set : A:\402iseq.001  
Output Set: N:\CRF3\05032001\I836911.raw

128	TTTGTGGAAT	CTGCAAGTGG	ATATTTGCT	AGCTTTGAGG	ATTTGTTGG	GAAACGGGAT	540
129	TACATATAAA	AAGCAGACAG	CAGCATTCCC	AGAAACTCT	TTGTGATGTT	TGCATTCAAG	600
130	TCACAGAGT	GAACATTCCC	TTTCATAGAG	CAGGTTGAA	ACACACTTT	TGATGTATCT	660
131	GGATGTGGAC	ATTCGAGCG	CTTCAGGCC	TAAGGTGAAA	AGGAAATATC	TTCCTGAA	720
132	AACTAGACAG	AAGCATTCTC	AGAAACTTAT	TTGTGATGTT	CGCCCTCAAC	TAACAGTGT	780
133	GAAGCTTTCT	TTTGATAGAG	GCAGTTTGAA	AAACACTCTT	TGTGAATCT	GCAAGTGGAT	840
134	ATTGTCTAG	CTTGAGGAT	TTCTTGAA	ACGGGATTAC	ATATAAAAAG	CAGACAGCAG	900
135	CATTCCCAGA	ATCTGTTTG	TGATGTTGC	ATTCAAGTCA	CAGAGTGAA	CATTCCCTT	960
136	CAGAGAGCAG	GTGGAAACAC	TCTTTTATA	GTATCTGGAT	GTGGACATT	GGAGCGCTT	1020
137	CAGGGGGGAT	CCTCTAGAA	TCCT				1044

141 (2) INFORMATION FOR SEQ ID NO: 3:

143 (i) SEQUENCE CHARACTERISTICS:  
 144 (A) LENGTH: 2492 base pairs  
 145 (B) TYPE: nucleic acid  
 146 (C) STRANDEDNESS: single  
 147 (D) TOPOLOGY: linear  
 149 (ii) MOLECULE TYPE: Genomic DNA  
 150 (iii) HYPOTHETICAL: NO  
 C--> 151 (iv) ANTI-SENSE: NO  
 W--> 152 (v) FRAGMENT TYPE:  
 153 (vi) ORIGINAL SOURCE:  
 154 (ix) FEATURE:  
 156 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

158	CTGCAGCTGG	GGGTCTCCAA	TCAGGCAGGG	GCCCCTTA	ACTCAGATGG	GGTGGCCGAG	60
159	TAGGGGAAGG	GGGTGCAAGG	TGCACTGAGTG	GACACAGCTG	TAGGACTACC	TGGGGGCTGT	120
160	GGATCTATGG	GGGTGGGGAG	AAGCCCAGTG	ACAGTGCCTA	GAAGAGACAA	GGTGGCCTGA	180
161	GAGGGTCTGA	GGAACATAGA	GCTGCCATG	TTGGGCCAG	GTCTCAAGCA	GGAAAGTGAGG	240
162	AATGGGACAG	GCTTGAGGAT	ACTCTACTCA	GTAGCCAGGA	TAGCAAGGAG	GGCTTGGGGT	300
163	TGCTATCCTG	GGGTTCAACC	CCCCCAGGTTG	AAAGGCCCTGG	GGGAGATGGT	CCCAGGACAT	360
164	ATTACAATGG	ACACAGGAGG	TTGGGACACC	TGGAGTCACC	AAACAAAACC	ATGCCAAGAG	420
165	AGACCATGAG	TAGGGGTGTC	CAGTCCAGCC	CTCTGACTGA	GCTGCATTGT	TCAAATCCAA	480
166	AGGGCCCCCTG	CTGCCACCTA	GTGGCTGATG	GCATCCACAT	GACCCCTGGGC	CACACGCGTT	540
167	TAGGGTCTCT	GTGAAGACCA	AGATCCTGT	TACATTGAAC	GACTCCTAAA	TGAGCAGAGA	600
168	TTTCCACCTA	TCGAAACAA	TCACATAAAA	TCCATCCTGG	AAAAGCCTG	GGGGATGGCA	660
169	CTAAGGCTAG	GGATAGGGTG	GGATGAAGAT	TATAGTTACA	GTAAGGGTT	TAGGGTTAGG	720
170	GATCAACGTT	GTTAGGGAGT	TAGGGATACA	GTAGGGTACC	GGTAGGGTTA	GGGGTTAGGG	780
171	TTAGGGTTA	GGGGTTAGGT	TAGGGTTAGG	GTTAGGGTTA	GGGGTTAGGG	GTTAGGGTTA	840
172	GGGTTAGGTT	TTGGGGTGGC	GTATTTGGT	CTTATACGCT	GTGTTCCACT	GGCAATGAAA	900
173	AGAGTTCTTG	TTTTCCCTTC	AGCAATTGT	CATTTTAA	AGAGTTAGC	AATTCTAACAA	960
174	GATATAGACC	AGCTGTGCTA	TCTCATTGTG	GTTCATTA	GTAACCCACAT	TGTGGTTCA	1020
175	ATGTGTTAC	TTGCCATCTG	TAGATCTCT	TTGCCTGAGG	TGTCTGTTCA	GATGTGTGT	1080
176	CATTCTTGN	NTTNGGCTG	TTAACCTAT	GTGTTAGTT	TAATAATT	TTATATATT	1140
177	GAAGACAAAT	CTTCTCAGA	TGTGATTTG	CAAATATTTC	TTCAATATGA	GGCTTGCTTT	1200
178	TGTCTCTAAC	AAGGTCTCTT	CAGAGATAAC	TAAATATAA	GAAATCCACA	CTGTCACCTC	1260
179	TTTGTGTAT	ATCTACCTTT	TGTGTCATT	GTTAAAATTC	ATTACCAAAC	CCAAAGGCAG	1320
180	ATAGCTTTTC	TTCTATTGTT	TCTCTAGAA	ATTTGTATA	TTTGCAATT	TTAGTGTAAAG	1380
181	GATGATTTG	AGTGATTATT	TGTGTAAGT	GTAAAGTTT	CGTCTATATC	CATATCATT	1440
182	CTTATGGTT	CCAATTAATC	GTTCCTCAC	TATTTTGGG	AAAGACACAG	GATAGTGGGC	1500
183	TTGTTAGAG	TAGATAGGTA	GCTAGACATG	AACAGGAGGG	GGCCTCCTGG	AAAAGGGAAA	1560

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/09/836,911

DATE: 05/03/2001  
TIME: 15:56:14

Input Set : A:\402iseq.001  
Output Set: N:\CRF3\05032001\I836911.raw

184	GTCTGGGAAG	GCTCACCTGG	AGGACCACCA	AAAATTACACA	TATTAGTAGC	ATCTCTAGTG	1620
185	CTGGAGTGG	TGGGCACCTG	TCAATTGTGG	GTAGGAGGGA	AAAGAGGTCC	TATGCAGAAA	1680
186	GAAACTCCCT	AGAACTCCTC	TGAAGATGCC	CCAATCATTC	ACTCTGCAAT	AAAAATGTCA	1740
187	GAATATTGCT	AGCTACATGC	TGAAAGGNN	AAAGGGGACA	TTCTTAAGTG	AAACCTGGCA	1800
188	CCATAAGTAC	AGATTAGGGC	AGAGAAAGGAC	ATTCAAAAGA	GGCAGGCGCA	GTAGGTACAA	1860
189	ACGTGATCGC	TGTCAGTGTG	CCTGGGATGG	CGGGAAGGAG	GCTGGTGCA	GAGTGGATTG	1920
190	GTATTGATCA	CCACACATAT	ACCTCAACCA	ACAGTGAGGA	GGTCCCACAA	GCCTAAGTGG	1980
191	GGCAAGTTGG	GGAGCTAAGG	CAGTAGCAGG	AAAACCAGAC	AAAGAAAACA	GGTGGAGACT	2040
192	TGAGACAGAG	GCAGGAATGT	GAAGAAATCC	AAAATAAAAT	TCCCTGCACA	GGACTCTTAG	2100
193	GCTGTTAAT	GCATCGCTCA	GTCCCACTCC	TCCCTATTT	TCTACAATAA	ACTCTTACA	2160
194	CTGTGTTCT	TTTCAATGAA	GTATCTGCC	ATCTTGAT	TGCCTCTGG	TGAAAATGTT	2220
195	TCTCCAAGT	TAAACAAGAA	CTGGGACATC	AGCTCTCCC	AGTAATAGCT	CCGTTTCAGT	2280
196	TTGAATTAC	AGAACTGATG	GGCTTAATAA	CTGGCGCTCT	GACTTTAGTG	GTGCAGGAGG	2340
197	CCGTCACACC	GGGACCAAGA	GTGCCCTGCC	TAGCCCCAT	CTGCCCGCAG	GTGGCGGCTG	2400
198	CCTCGACACT	GACAGCAATA	GGGTCCGGCA	GTGTCCCCAG	CTGCCAGCAG	GGGGCGTACG	2460
199	ACGACTACAC	TGTGAGCAAG	AGGGCCCTGC	AG			2492

201 (2) INFORMATION FOR SEQ ID NO: 4:  
 203 (i) SEQUENCE CHARACTERISTICS:  
 204 (A) LENGTH: 28 base pairs  
 205 (B) TYPE: nucleic acid  
 206 (C) STRANDEDNESS: single  
 207 (D) TOPOLOGY: linear  
 209 (ii) MOLECULE TYPE: Genomic DNA  
 210 (iii) HYPOTHETICAL: NO  
 211 (iv) ANTI-SENSE: NO  
 212 (v) FRAGMENT TYPE:  
 213 (vi) ORIGINAL SOURCE:  
 214 (ix) FEATURE:  
 216 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:  
 218 GGGGAATTCA TTGGGATGTT TCAGTTGA

28

220 (2) INFORMATION FOR SEQ ID NO: 5:  
 222 (i) SEQUENCE CHARACTERISTICS:  
 223 (A) LENGTH: 29 base pairs  
 224 (B) TYPE: nucleic acid  
 225 (C) STRANDEDNESS: single  
 226 (D) TOPOLOGY: linear  
 228 (ii) MOLECULE TYPE: Genomic DNA  
 229 (iii) HYPOTHETICAL: NO  
 230 (iv) ANTI-SENSE: NO  
 231 (v) FRAGMENT TYPE:  
 232 (vi) ORIGINAL SOURCE:  
 233 (ix) FEATURE:  
 235 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:  
 237 CGAAAGTCCC CCCTAGGAGA TCTTAAGGA

29

239 (2) INFORMATION FOR SEQ ID NO: 6:  
 241 (i) SEQUENCE CHARACTERISTICS:  
 242 (A) LENGTH: 47 base pairs  
 243 (B) TYPE: nucleic acid  
 244 (C) STRANDEDNESS: single

C--&gt;

W--&gt;

C--&gt;

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/09/836,911

DATE: 05/03/2001  
TIME: 15:56:14

Input Set : A:\402iseq.001  
Output Set: N:\CRF3\05032001\I836911.raw

245 (D) TOPOLOGY: linear  
W--> 247 (ii) MOLECULE TYPE: DNA  
248 (iii) HYPOTHETICAL: NO  
C--> 249 (iv) ANTI-SENSE: NO  
W--> 250 (v) FRAGMENT TYPE:  
251 (vi) ORIGINAL SOURCE:  
252 (ix) FEATURE:  
254 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:  
256 CCGCTTAATA CTCTGATGAG TCCGTGAGGA CGAAACGCTC TCGCACC 47  
260 (2) INFORMATION FOR SEQ ID NO: 7:  
262 (i) SEQUENCE CHARACTERISTICS:  
263 (A) LENGTH: 25 base pairs  
264 (B) TYPE: nucleic acid  
265 (C) STRANDEDNESS: single  
266 (D) TOPOLOGY: linear  
268 (ii) MOLECULE TYPE: Genomic DNA  
269 (iii) HYPOTHETICAL: NO  
C--> 270 (iv) ANTI-SENSE: NO  
W--> 271 (v) FRAGMENT TYPE:  
272 (vi) ORIGINAL SOURCE:  
273 (ix) FEATURE:  
275 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:  
277 CGATTTAAC TAAATTAGCC CGGGC 25  
280 (2) INFORMATION FOR SEQ ID NO: 8:  
282 (i) SEQUENCE CHARACTERISTICS:  
283 (A) LENGTH: 27 base pairs  
284 (B) TYPE: nucleic acid  
285 (C) STRANDEDNESS: single  
286 (D) TOPOLOGY: linear  
288 (ii) MOLECULE TYPE: Genomic DNA  
289 (iii) HYPOTHETICAL: NO  
C--> 290 (iv) ANTI-SENSE: NO  
W--> 291 (v) FRAGMENT TYPE:  
292 (vi) ORIGINAL SOURCE:  
293 (ix) FEATURE:  
295 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:  
297 TAAATTAAAT TAAATCGGGC CGGTGCA 27  
299 (2) INFORMATION FOR SEQ ID NO: 9:  
301 (i) SEQUENCE CHARACTERISTICS:  
302 (A) LENGTH: 69 base pairs  
303 (B) TYPE: nucleic acid  
304 (C) STRANDEDNESS: single  
305 (D) TOPOLOGY: linear  
307 (ii) MOLECULE TYPE: Genomic DNA  
310 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:  
312 ATG TAC AGG ATG CAA CTC CTG TCT TGC ATT GCA CTA AGT CTT GCA CTT 48  
313 Met Tyr Arg Met Gln Leu Leu Ser Cys Ile Ala Leu Ser Leu Ala Leu  
W--> 315 GTC ACA AAC AGT GCA CCT ACT 69  
316 Val Thr Asn Ser Ala Pro Thr

(Per  
Sequence Rules,

→ Number

→ the  
amino  
acids

under every  
5 amino  
acids — do not  
use TAB codes  
between numbers 5/3/01

Please edit all subsequent sequences  
containing these errors

VERIFICATION SUMMARY  
PATENT APPLICATION: US/09/836,911

DATE: 05/03/2001  
TIME: 15:56:15

Input Set : A:\402iseg.001  
Output Set: N:\CRF3\05032001\I836911.raw

L:4 M:220 C: Keyword misspelled or invalid format, [(1) GENERAL INFORMATION:]  
 L:9 M:220 C: Keyword misspelled or invalid format, [(ii) TITLE OF INVENTION:]  
 L:29 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]  
 L:30 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]  
 L:37 M:220 C: Keyword misspelled or invalid format, [(vii) PRIOR APPLICATION DATA:]  
 L:42 M:220 C: Keyword misspelled or invalid format, [(vii) PRIOR APPLICATION DATA:]  
 L:47 M:220 C: Keyword misspelled or invalid format, [(vii) PRIOR APPLICATION DATA:]  
 L:73 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]  
 L:78 M:246 W: Invalid value of Alpha Sequence Header Field, [FEATURE:], SeqNo=1  
 L:74 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=1  
 L:113 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]  
 L:118 M:246 W: Invalid value of Alpha Sequence Header Field, [FEATURE:], SeqNo=2  
 L:114 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=2  
 L:151 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]  
 L:156 M:246 W: Invalid value of Alpha Sequence Header Field, [FEATURE:], SeqNo=3  
 L:152 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=3  
 L:211 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]  
 L:216 M:246 W: Invalid value of Alpha Sequence Header Field, [FEATURE:], SeqNo=4  
 L:212 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=4  
 L:230 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]  
 L:235 M:246 W: Invalid value of Alpha Sequence Header Field, [FEATURE:], SeqNo=5  
 L:231 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=5  
 L:249 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]  
 L:254 M:246 W: Invalid value of Alpha Sequence Header Field, [FEATURE:], SeqNo=6  
 L:247 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=6  
 L:250 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=6  
 L:270 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]  
 L:275 M:246 W: Invalid value of Alpha Sequence Header Field, [FEATURE:], SeqNo=7  
 L:271 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=7  
 L:290 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]  
 L:295 M:246 W: Invalid value of Alpha Sequence Header Field, [FEATURE:], SeqNo=8  
 L:291 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=8  
 L:308 M:220 C: Keyword misspelled or invalid format, [(D) OTHER INFORMATION:]  
 L:308 M:220 C: Keyword misspelled or invalid format, Poss data loss, Seq 9, (D) OTHER INFORMATION:  
 L:315 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:9  
 L:339 M:220 C: Keyword misspelled or invalid format, [(H) DOCUMENT NUMBER:]  
 L:433 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]  
 L:438 M:246 W: Invalid value of Alpha Sequence Header Field, [FEATURE:], SeqNo=11  
 L:434 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=11  
 L:452 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]  
 L:457 M:246 W: Invalid value of Alpha Sequence Header Field, [FEATURE:], SeqNo=12  
 L:453 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=12  
 L:471 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]  
 L:472 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=13  
 L:512 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]  
 L:513 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=14  
 L:553 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]  
 L:554 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=15

VERIFICATION SUMMARY  
PATENT APPLICATION: US/09/836,911

DATE: 05/03/2001  
TIME: 15:56:15

Input Set : A:\402iseq.001  
Output Set: N:\CRF3\05032001\I836911.raw

L:593 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]  
L:594 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=16  
L:979 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]  
L:980 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=17  
L:1713 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]  
L:1714 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=18  
L:1734 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]  
L:1735 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=19  
L:1764 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]  
L:1765 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=20  
L:1789 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]  
L:1790 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=21  
L:1813 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]  
L:1814 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=22  
L:1837 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]  
L:1838 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=23  
L:1866 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]  
L:1867 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=24  
L:1896 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]  
L:1897 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=25  
L:1914 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]  
L:1915 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=26  
L:1932 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]  
L:1933 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=27  
L:1950 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]  
L:1951 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=28  
L:1968 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]  
L:1969 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=29  
L:1987 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]  
L:1988 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=30  
L:2005 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]  
L:2006 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=31  
L:2023 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]  
L:2024 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=32  
L:2041 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]  
L:2042 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=33  
L:2059 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]  
L:2060 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=34